BIOTECHNOLOGY
SYSTEMS
BRANCH

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _10/016,516_
Source: _OIPE_
Date Processed by STIC: _4/11/2002_

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2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
 PATENTIN 2.1 e-mail help: **patin21help@uspto.gov** or phone 703-306-4119 (R. Wax)
 PATENTIN 3.0 e-mail help: **patin3help@uspto.gov** or phone 703-306-4119 (R. Wax)

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Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<**http://www.uspto.gov/ebc/efs/downloads/documents.htm**> , **EFS Submission User Manual** - ePAVE)
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            Or
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Revised 01/29/2002

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: _10/.016, 876_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ___ Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 ___ Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ___ Misaligned Amino
Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 ___ Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 ___ Variable Length

Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ___ PatentIn 2.0
"bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 ___ Skipped Sequences
(OLD RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ___ Skipped Sequences
(NEW RULES)

Sequence(s) _____ missing. If Intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 ___ Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.

10 ___ Invalid <213>
Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 ___ Use of <220>

Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12 ___ PatentIn 2.0
"bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ___ Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001

OIPE

RAW SEQUENCE LISTING   DATE: 04/11/2002
PATENT APPLICATION: US/10/016,516   TIME: 13:20:26

Input Set : A:\EP.txt   Does Not Comply
Output Set: N:\CRF3\04112002\J016516.raw   Corrected Diskette Needed

```
   3 <110> APPLICANT: Houtzager, Erwin
   4        Vijn, Irma Maria Caecilia
   5        Sijmons, Peter Christiaan
   7 <120> TITLE OF INVENTION: A Structure for Presenting Desired Peptide Sequences
   9 <130> FILE REFERENCE: 2183-5208US
  11 <140> CURRENT APPLICATION NUMBER: US 10/016,516
  12 <141> CURRENT FILING DATE: 2001-12-10
E-->  14 <160> NUMBER OF SEQ ID NOS: (17)/8 (P.24)
  16 <170> SOFTWARE: PatentIn version 3.1
```

ERRORED SEQUENCES

```
  18 <210> SEQ ID NO: 1
  19 <211> LENGTH: 291
  20 <212> TYPE: DNA
  21 <213> ORGANISM: Artificial Sequence
  23 <220> FEATURE:
  24 <223> OTHER INFORMATION: Description of Artificial Sequence: 5' end of exemplary
maximal
  25        primary scaffold.
  27 <220> FEATURE:
  28 <221> NAME/KEY: misc_feature
  29 <222> LOCATION: (79)..(93)
  30 <223> OTHER INFORMATION: The nucleotide at each of positions 79-93 may be any
nucleotide.
  32 <220> FEATURE:
  33 <221> NAME/KEY: misc_feature
  34 <222> LOCATION: (157)..(159)
  35 <223> OTHER INFORMATION: The nucleotide at each of positions 157-159 may be any
nucleotide.
  37 <220> FEATURE:
  38 <221> NAME/KEY: misc_feature
  39 <222> LOCATION: (214)..(222)
  40 <223> OTHER INFORMATION: The nucleotide at each of positions 214-222 may be any
nucleotide.
  42 <400> SEQUENCE: 1    (GLOBAL ERRORS) See Error Summary Sheet, item 1
E-->  43 aat  gtg  aaa  ctg  gtt  gaa  aaa  ggt  ggc  aat  ttc  gtc  gaa
      44 aac  gat  gac  gat  ctt            54
      47 Asn  Val  Lys  Leu  Val  Glu  Lys  Gly  Gly  Asn  Phe  Val  Glu  Asn  Asp  Asp
W-->  48 Asp  Leu
W-->  49                                              1                    5
E-->  50 10               15
E-->  52 aag  ctc  acg  tgc  cgt  gct  gaa  ggt  nnn  nnn  nnn  nnn  nnn
```

```
      53 tac   tgc   atg   ggt   tgg   108
W--> 55 Lys  Leu  Thr  Cys  Arg  Ala  Glu  Gly  Xaa  Xaa  Xaa  Xaa  Xaa  Tyr  Cys  Met
W--> 56 Gly  Trp
```

Sameena

RAW SEQUENCE LISTING   DATE: 04/11/2002
PATENT APPLICATION: US/10/016,516   TIME: 13:20:26

Input Set : A:\EP.txt
Output Set: N:\CRF3\04112002\J016516.raw   *same*

```
W--> 57                                                                    20
E--> 58 25                    30                     35
E--> 60 ttc   cgt   cag   gcg   ccg   aac   gac   gac   agt   act   aac   gtg   gcc
W--> 61 acg   atc   tta   nnn   ggg   162
     63 Phe   Arg   Gln   Ala   Pro   Asn   Asp   Asp   Ser   Thr   Asn   Val   Ala   Thr   Ile   Leu
W--> 64 Xaa   Gly
W--> 65                                                             40                     45
E--> 66 50
E--> 68 agc   acg   tac   tac   ggt   gac   tcc   gtc   aaa   gag   cgc   ttc   gat
W--> 69 atc   cgt   cgc   gac   nnn   216
     71 Ser   Thr   Tyr   Tyr   Gly   Asp   Ser   Val   Lys   Glu   Arg   Phe   Asp   Ile   Arg   Arg
W--> 72 Asp   Xaa
W--> 73                                                       55                     60
E--> 74 65                    70
E--> 76 nnn   nnn   aac   acc   gtt   acc   tta   tcg   atg   gac   gat   ctg   caa
     77 ccg   gaa   gac   tct   gca   270
W--> 79 Xaa   Xaa   Asn   Thr   Val   Thr   Leu   Ser   Met   Asp   Asp   Leu   Gln   Pro   Glu   Asp
W--> 80 Ser   Ala
W--> 81                                                                           75
E--> 82 80                    85                     90
E--> 85 gaa   tac   aat   tgt   gca   ggt   tct
     86 291
     88 Glu   Tyr   Asn   Cys   Ala   Gly   Ser
W--> 89                       95
     91 <210> SEQ ID NO: 2
     92 <211> LENGTH: 42
     93 <212> TYPE: DNA
     94 <213> ORGANISM: Artificial Sequence
     96 <220> FEATURE:
     97 <223> OTHER INFORMATION: Description of Artificial Sequence: 3' end of exemplary
maximal
     98       primary scaffold.       *same*
    100 <400> SEQUENCE: 2
E--> 102 tac   cac   tac   cgt   ggt   cag   ggt   acc   gac   gtt   acc   gtc   tcg
    103 tcg         42
    105 Tyr   His   Tyr   Arg   Gly   Gln   Gly   Thr   Asp   Val   Thr   Val   Ser   Ser
W--> 106                                       1              5                    10
    110 <210> SEQ ID NO: 3
    111 <211> LENGTH: 405
    112 <212> TYPE: DNA
    113 <213> ORGANISM: Artificial Sequence
    115 <220> FEATURE:
    116 <223> OTHER INFORMATION: Description of Artificial Sequence: Scaffold with VHH 1MEL
CDR
    117       regions.
    119 <400> SEQUENCE: 3
E--> 120 aat   gtg   aaa   ctg   gtt   gaa   aaa   ggt   ggc   aat   ttc   gtc   gaa
    121 aac   gat   gac   gat   ctt   54
    123 Asn   Val   Lys   Leu   Val   Glu   Lys   Gly   Gly   Asn   Phe   Val   Glu   Asn   Asp   Asp
W--> 124 Asp   Leu
W--> 125                                                     1                      5
```

Misaligned amino acid numbers
GLOBAL error (see item 3 on Error Summary Sheet)

same error

```
RAW SEQUENCE LISTING              DATE: 04/11/2002
PATENT APPLICATION:  US/10/016,516    TIME: 13:20:26

         Input Set : A:\EP.txt
         Output Set: N:\CRF3\04112002\J016516.raw
```

```
E--> 126 10                        15
E--> 128 aag   ctc   acg   tgc   cgt   gct   gaa   ggt   tac   acc   att   ggc   ccg
     129 tac   tgc   atg   ggt   tgg         108
     131 Lys   Leu   Thr   Cys   Arg   Ala   Glu   Gly   Tyr   Thr   Ile   Gly   Pro   Tyr   Cys   Met
W--> 132 Gly   Trp
W--> 133                                                                   20
E--> 134 25                  30                  35
E--> 136 ttc   cgt   cag   gcg   ccg   aac   gac   gac   agt   act   aac   gtg   gcc
     137 acg   atc   aac   atg   ggt         162
     139 Phe   Arg   Gln   Ala   Pro   Asn   Asp   Asp   Ser   Thr   Asn   Val   Ala   Thr   Ile   Asn
W--> 140 Met   Gly
W--> 141                                                         40                      45
E--> 142 50
E--> 144 ggc   ggt   att   acg   tac   tac   ggt   gac   tcc   gtc   aaa   gag   cgc
     145 ttc   gat   atc   cgt   cgc         216
     147 Gly   Gly   Ile   Thr   Tyr   Tyr   Gly   Asp   Ser   Val   Lys   Glu   Arg   Phe   Asp   Ile
W--> 148 Arg   Arg
W--> 149                                                         55                      60
E--> 150 65                        70
E--> 152 gac   aac   gcg   tcc   aac   acc   gtt   acc   tta   tcg   atg   gac   gat
     153 ctg   caa   ccg   gaa   gac         270
     155 Asp   Asn   Ala   Ser   Asn   Thr   Val   Thr   Leu   Ser   Met   Asp   Asp   Leu   Gln   Pro
W--> 156 Glu   Asp
W--> 157                                                                   75
E--> 158 80                  85                  90
E--> 160 tct   gca   gaa   tac   aat   tgt   gca   ggt   gat   tct   acc   att   tac
     161 gcg   agc   tat   tat   gaa         324
     163 Ser   Ala   Glu   Tyr   Asn   Cys   Ala   Gly   Asp   Ser   Thr   Ile   Tyr   Ala   Ser   Tyr
W--> 164 Tyr   Glu
W--> 165                                                                   95
E--> 166 100                 105
E--> 168 tgt   ggt   cat   ggc   ctg   agt   acc   ggc   ggt   tac   ggc   tac   gat
     169 agc   cac   tac   cgt   ggt         378
     171 Cys   Gly   His   Gly   Leu   Ser   Thr   Gly   Gly   Tyr   Gly   Tyr   Asp   Ser   His   Tyr
W--> 172 Arg   Gly
W--> 173                                                                   110
E--> 174 115                 120                 125
E--> 177 cag   ggt   acc   gac   gtt   acc   gtc   tcg   tcg
     178 405
     180 Gln   Gly   Thr   Asp   Val   Thr   Val   Ser   Ser
W--> 181                                             130             135
     183 <210> SEQ ID NO: 4
     184 <211> LENGTH: 422
     185 <212> TYPE: DNA
     186 <213> ORGANISM: Artificial Sequence
     188 <220> FEATURE:
     189 <223> OTHER INFORMATION: Description of Artificial Sequence: Scaffold with VHH 1BZQ
CDR
     190       regions.
     192 <400> SEQUENCE: 4
```

Input Set : A:\EP.txt
Output Set: N:\CRF3\04112002\J016516.raw

```
E--> 193 aat   gtg   aaa   ctg   gtt   gaa   aaa   ggt   ggc   aat   ttc   gtc   gaa
     194 aac   gat   gac   gat   ctt         54
     196 Asn   Val   Lys   Leu   Val   Glu   Lys   Gly   Gly   Asn   Phe   Val   Glu   Asn   Asp   Asp
W--> 197 Asp   Leu
W--> 198                                                 1                       5
E--> 199 10                      15
E--> 201 aag   ctc   acg   tgc   cgt   gct   agc   ggt   tac   gcc   tac   acg   tat
     202 atc   tac   atg   ggt   tgg         108
     204 Lys   Leu   Thr   Cys   Arg   Ala   Ser   Gly   Tyr   Ala   Tyr   Thr   Tyr   Ile   Tyr   Met
W--> 205 Gly   Trp
W--> 206                                                                  20
E--> 207 25                30                35
E--> 209 ttc   cgt   cag   gcg   ccg   aac   gac   gac   agt   act   aac   gtg   gcc
     210 acc   atc   gac   tcg   ggt         162
     212 Phe   Arg   Gln   Ala   Pro   Asn   Asp   Asp   Ser   Thr   Asn   Val   Ala   Thr   Ile   Asp
W--> 213 Ser   Gly
W--> 214                                                 40                      45
E--> 215 50
E--> 217 ggc   ggc   ggt   acc   ctg   tac   ggt   gac   tcc   gtc   aaa   gag   cgc
     218 ttc   gat   atc   cgt   cgc         216
     220 Gly   Gly   Gly   Thr   Leu   Tyr   Gly   Asp   Ser   Val   Lys   Glu   Arg   Phe   Asp   Ile
W--> 221 Arg   Arg
W--> 222                                                 55                      60
E--> 223 65                      70
E--> 225 gac   aaa   ggc   tcc   aac   acc   gtt   acc   tta   tcg   atg   gac   gat
     226 ctg   caa   ccg   gaa   gac         270
     228 Asp   Lys   Gly   Ser   Asn   Thr   Val   Thr   Leu   Ser   Met   Asp   Asp   Leu   Gln   Pro
W--> 229 Glu   Asp
W--> 230                                                                  75
E--> 231 80                85                90
E--> 233 tct   gca   gaa   tac   aat   tgt   gca   gcg   ggt   ggc   tac   gaa   ctg
     234 cgc   gac   cgc   acc   tac         324
     236 Ser   Ala   Glu   Tyr   Asn   Cys   Ala   Ala   Gly   Gly   Tyr   Glu   Leu   Arg   Asp   Arg
W--> 237 Thr   Tyr
W--> 238                                                                  95
E--> 239 100               105
E--> 241 ggt   cag   cgt   ggt   cag   ggt   acc   gac   gtt   acc   gtc   tcg   tcg
E--> 242 383
     244 Gly   Gln   Arg   Gly   Gln   Gly   Thr   Asp   Val   Thr   Val   Ser   Ser
W--> 245                                                 110                     115
E--> 246 120
     248 <210> SEQ ID NO: 5
     249 <211> LENGTH: 351
     250 <212> TYPE: DNA
     251 <213> ORGANISM: Artificial Sequence
     253 <220> FEATURE:
     254 <223> OTHER INFORMATION: Description of Artificial Sequence: Scaffold with VHH 1HCV
CDR
     255       regions.
     257 <400> SEQUENCE: 5
```

```
E--> 258 aat   gtg   aaa   ctg   gtt   gaa   aaa   ggt   ggc   aat   ttc   gtc   gaa
     259 aac   gat   gac   gat   ctt         54
     261 Asn   Val   Lys   Leu   Val   Glu   Lys   Gly   Gly   Asn   Phe   Val   Glu   Asn   Asp   Asp
W--> 262 Asp   Leu
W--> 263                                                       1                         5
E--> 264 10                15
E--> 266 aag   ctc   acg   tgc   cgt   gct   gaa   ggt   cgt   acg   ggt   tcg   acc
     267 tac   gat   atg   ggt   tgg         108
     269 Lys   Leu   Thr   Cys   Arg   Ala   Glu   Gly   Arg   Thr   Gly   Ser   Thr   Tyr   Asp   Met
W--> 270 Gly   Trp
W--> 271                                                                         20
E--> 272 25                30                      35
E--> 274 ttc   cgt   cag   gcg   ccg   aac   gac   gac   agt   act   aac   gtg   gcc
     275 acg   atc   aac   tgg   gat         162
     277 Phe   Arg   Gln   Ala   Pro   Asn   Asp   Asp   Ser   Thr   Asn   Val   Ala   Thr   Ile   Asn
W--> 278 Trp   Asp
W--> 279                                                       40                        45
E--> 280 50
E--> 282 agc   gcc   cgt   acg   tac   tac   ggt   gac   tcc   gtc   aaa   gag   cgc
     283 ttc   gat   atc   cgt   cgc         216
     285 Ser   Ala   Arg   Thr   Tyr   Tyr   Gly   Asp   Ser   Val   Lys   Glu   Arg   Phe   Asp   Ile
W--> 286 Arg   Arg
W--> 287                                                                         55
E--> 288 60          .           65                      70
E--> 290 gac   aat   gcc   tcc   aac   acc   gtt   acc   tta   tcg   atg   gac   gat
     291 ctg   caa   ccg   gaa   gac         270
     293 Asp   Asn   Ala   Ser   Asn   Thr   Val   Thr   Leu   Ser   Met   Asp   Asp   Leu   Gln   Pro
W--> 294 Glu   Asp
W--> 295                                                                         75
E--> 296 80                85                      90
E--> 298 tct   gca   gaa   tac   aat   tgt   gca   ggt   ggt   gaa   ggc   ggc   acc
     299 tgg   gat   agc   cgt   ggt         324
     302 Ser   Ala   Glu   Tyr   Asn   Cys   Ala   Gly   Gly   Glu   Gly   Gly   Thr   Trp   Asp   Ser
W--> 303 Arg   Gly
W--> 304                                                                         95
E--> 305 100               105
E--> 308 cag   ggt   acc   gac   gtt   acc   gtc   tcg   tcg
     309 351
     311 Gln   Gly   Thr   Asp   Val   Thr   Val   Ser   Ser
W--> 312                                                 110               115
     340 <210> SEQ ID NO: 8
     341 <211> LENGTH: 144
     342 <212> TYPE: PRT
     343 <213> ORGANISM: IF2X - Single Domain Camelid Antibody Cab-Ca05
     345 <220> FEATURE:
     346 <221> NAME/KEY: misc_feature
     347 <222> LOCATION: (7)
     348 <223> OTHER INFORMATION: The 'Xaa' indicator at position 7 indicates the absence of
an amino
     349       acid residue.
```

```
351 <220> FEATURE:
352 <221> NAME/KEY: misc_feature
353 <222> LOCATION: (10)..(11)
354 <223> OTHER INFORMATION: The 'Xaa' indicators at positions 10-11 indicate the absence
of
355       amino acid residues.
357 <220> FEATURE:
358 <221> NAME/KEY: misc_feature
359 <222> LOCATION: (13)
360 <223> OTHER INFORMATION: The 'Xaa' indicator at position 13 indicates the absence of
an amino
361       acid residue.
363 <220> FEATURE:
364 <221> NAME/KEY: misc_feature
365 <222> LOCATION: (33)..(37)
366 <223> OTHER INFORMATION: The 'Xaa' indicators at positions 33-37 indicate the absence
of
367       amino acid residues.
369 <220> FEATURE:
370 <221> NAME/KEY: misc_feature
371 <222> LOCATION: (49)
372 <223> OTHER INFORMATION: The 'Xaa' indicator at position 49 indicates the absence of
an amino
373       acid residue.
375 <220> FEATURE:
376 <221> NAME/KEY: misc_feature
377 <222> LOCATION: (54)..(55)
378 <223> OTHER INFORMATION: The 'Xaa' indicators at positions 54-55 indicate the absence
of
379       amino acid residues.
381 <220> FEATURE:
382 <221> NAME/KEY: misc_feature
383 <222> LOCATION: (65)..(66)
384 <223> OTHER INFORMATION: The 'Xaa' indicators at positions 65-66 indicate the absence
of
385       amino acid residues.
387 <220> FEATURE:
388 <221> NAME/KEY: misc_feature
389 <222> LOCATION: (68)..(69)
390 <223> OTHER INFORMATION: The 'Xaa' indicators at positions 68-69 indicate the absence
of
391       amino acid residues.
393 <220> FEATURE:
394 <221> NAME/KEY: misc_feature
395 <222> LOCATION: (101)
396 <223> OTHER INFORMATION: The 'Xaa' indicator at position 101 indicates the absence of
an
397       amino acid residue.
399 <220> FEATURE:
400 <221> NAME/KEY: misc_feature
401 <222> LOCATION: (103)
402 <223> OTHER INFORMATION: The 'Xaa' indicator at position 103 indicates the absence of
an
```

```
403       amino acid residue.
405 <220> FEATURE:
406 <221> NAME/KEY: misc_feature
407 <222> LOCATION: (140)
408 <223> OTHER INFORMATION: The 'Xaa' indicator at position 140 indicates the absence of
an
```

```
                 Input Set : A:\EP.txt
                 Output Set: N:\CRF3\04112002\J016516.raw
     409         amino acid residue.  same  format errors as described
     411   <400> SEQUENCE: 8                            on pp. 1,3
W--> 412 Gln  Val  Gln  Leu  Val  Glu  Xaa  Ser  Gly  Xaa  Xaa  Gly  Xaa  Gly  Ser  Val
E--> 413 Gln  Ala
E--> 414                                                                     1
E--> 415 5                        10                      15
W--> 417 Gly  Gly  Ser  Leu  Arg  Leu  Ser  Cys  Ala  Ala  Ser  Gly  Tyr  Thr  Xaa  Xaa
E--> 418 Xaa  Xaa
E--> 420 20              25              30                      35
W--> 422 Xaa  Val  Ser  Thr  Tyr  Cys  Met  Gly  Trp  Phe  Arg  Gln  Xaa  Ala  Pro  Gly
E--> 423 Lys  Xaa
E--> 424                                                                          40
E--> 425 45              50
W--> 427 Xaa  Glu  Arg  Glu  Gly  Val  Ala  Thr  Ile  Leu  Xaa  Xaa  Gly  Xaa  Xaa  Gly
E--> 428 Ser  Thr
E--> 429                                                      55
E--> 430 60              65              70
     432 Tyr  Tyr  Gly  Asp  Ser  Val  Lys  Gly  Arg  Phe  Thr  Ile  Ser  Gln  Asp  Asn
E--> 433 Ala  Lys
E--> 435 75              80              85              90
W--> 437 Asn  Thr  Val  Tyr  Leu  Gln  Met  Asn  Ser  Leu  Xaa  Lys  Xaa  Pro  Glu  Asp
E--> 438 Thr  Ala
E--> 439                                                      95
E--> 440 100             105
     442 Ile  Tyr  Tyr  Cys  Ala  Gly  Ser  Thr  Val  Ala  Ser  Thr  Gly  Trp  Cys  Ser
E--> 443 Arg  Leu
E--> 444                                                      110
E--> 445 115             120             125
W--> 447 Arg  Pro  Tyr  Asp  Tyr  His  Tyr  Arg  Gly  Gln  Gly  Thr  Gln  Xaa  Val  Thr
E--> 448 Val  Ser
E--> 449                                                      130
E--> 450 135             140
     452   <210> SEQ ID NO: 9
     453   <211> LENGTH: 144
     454   <212> TYPE: PRT
     455   <213> ORGANISM: 1QD0 - Camelid Heavy Chain Variable Domain
     457   <220> FEATURE:
     458   <221> NAME/KEY: misc_feature
     459   <222> LOCATION: (7)
     460   <223> OTHER INFORMATION: The 'Xaa' indicator at position 7 indicates the absence of
an amino
     461         acid residue.
     463   <220> FEATURE:
     464   <221> NAME/KEY: misc_feature
     465   <222> LOCATION: (10)..(11)
     466   <223> OTHER INFORMATION: The 'Xaa' indicators at positions 10-11 indicate the absence
of
     467         amino acid residues.
     469   <220> FEATURE:
     470   <221> NAME/KEY: misc_feature
     471   <222> LOCATION: (13)
```

```
    472 <223> OTHER INFORMATION: The 'Xaa' indicator at position 13 indicates the absence of
an amino
    473       acid residue.
    475 <220> FEATURE:
    476 <221> NAME/KEY: misc_feature
    477 <222> LOCATION: (33)..(34)
    478 <223> OTHER INFORMATION: The 'Xaa' indicators at positions 33-34 indicate the absence
    479       of amino acid residues.
    481 <220> FEATURE:
    482 <221> NAME/KEY: misc_feature
    483 <222> LOCATION: (49)
    484 <223> OTHER INFORMATION: The 'Xaa' indicator at position 49 indicates the absence of
    485       an amino acid residue.
    487 <220> FEATURE:
    488 <221> NAME/KEY: misc_feature
    489 <222> LOCATION: (54)..(55)
    490 <223> OTHER INFORMATION: The 'Xaa' indicators at positions 54-55 indicate the absence
    491       of amino acid residues .
    493 <220> FEATURE:
    494 <221> NAME/KEY: misc_feature
    495 <222> LOCATION: (68)..(69)
    496 <223> OTHER INFORMATION: The 'Xaa' indicators at positions 68-69 indicate the absence
    497       of amino acid residues.
    499 <220> FEATURE:
    500 <221> NAME/KEY: misc_feature
    501 <222> LOCATION: (101)
    502 <223> OTHER INFORMATION: The 'Xaa' indicator at position 101 indicates the absence of
    503       an amino acid residue.
    505 <220> FEATURE:
    506 <221> NAME/KEY: misc_feature
    507 <222> LOCATION: (103)
    508 <223> OTHER INFORMATION: The 'Xaa' indicator at position 103 indicates the absence of
    509       an amino acid residue.
    511 <220> FEATURE:
    512 <221> NAME/KEY: misc_feature
    513 <222> LOCATION: (124)..(126)
    514 <223> OTHER INFORMATION: The 'Xaa' indicators at positions 124-126 indicate the
    515       absence of amino acid residues.
    517 <220> FEATURE:
    518 <221> NAME/KEY: misc_feature
    519 <222> LOCATION: (140)
    520 <223> OTHER INFORMATION: The 'Xaa' indicator at position 140 indicates the absence of
    521       an amino acid residue.
    523 <400> SEQUENCE: 9
W--> 524 Gln  Val  Gln  Leu  Gln  Glu  Xaa  Ser  Gly  Xaa  Xaa  Gly  Xaa  Gly  Leu  Val
E--> 525 Gln  Ala
E--> 526                                                        1                    5
E--> 527 10                   15
W--> 529 Gly  Gly  Ser  Leu  Arg  Leu  Ser  Cys  Ala  Ala  Ser  Gly  Arg  Ala  Xaa  Xaa
E--> 530 Ala  Ser
```

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Input Set : A:\EP.txt
Output Set: N:\CRF3\04112002\J016516.raw

```
E--> 531                                                        20
E--> 532 25               30                35
W--> 534 Gly His Gly His Tyr Gly Met Gly Trp Phe Arg Gln Xaa Val Pro Gly
E--> 535 Lys Xaa
E--> 537 40               45                50
W--> 539 Xaa Glu Arg Glu Phe Val Ala Ala Ile Arg Trp Ser Gly Xaa Xaa Lys
E--> 540 Glu Thr
E--> 541                                                        55
E--> 542 60               65                70
     544 Trp Tyr Lys Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
E--> 545 Ala Lys
E--> 547 75               80                85          90
W--> 549 Thr Thr Val Tyr Leu Gln Met Asn Ser Leu Xaa Lys Xaa Gly Glu Asp
E--> 550 Thr Ala
E--> 551                                                        95
E--> 552 100              105
W--> 554 Val Tyr Tyr Cys Ala Ala Arg Pro Val Arg Val Ala Asp Ile Ser Xaa
E--> 555 Xaa Xaa
E--> 557 110              115               120         125
W--> 559 Leu Pro Val Gly Phe Asp Tyr Trp Gly Gln Gly Thr Gln Xaa Val Thr
E--> 560 Val Ser
E--> 561                                                        130
E--> 562 135              140
     564 <210> SEQ ID NO: 10
     565 <211> LENGTH: 144
     566 <212> TYPE: PRT
     567 <213> ORGANISM: 8FAB - Heavy Chain from Human Igg1
     569 <220> FEATURE:
     570 <221> NAME/KEY: misc_feature
     571 <222> LOCATION: (7)
     572 <223> OTHER INFORMATION: The 'Xaa' indicator at position 7 indicates the absence of
an amino
     573       acid residue.
     575 <220> FEATURE:
     576 <221> NAME/KEY: misc_feature
     577 <222> LOCATION: (10)..(11)
     578 <223> OTHER INFORMATION: The 'Xaa' indicators at positions 10-11 indicate the absence
of
     579       amino acid residues.
     581 <220> FEATURE:
     582 <221> NAME/KEY: misc_feature
     583 <222> LOCATION: (13)
     584 <223> OTHER INFORMATION: The 'Xaa' indicator at position 13 indicates the absence of
an amino
     585       acid residue.
     587 <220> FEATURE:
     588 <221> NAME/KEY: misc_feature
     589 <222> LOCATION: (33)..(37)
     590 <223> OTHER INFORMATION: The 'Xaa' indicators at positions 33-37 indicate the absence
of
     591       amino acid residues.
     593 <220> FEATURE:
     594 <221> NAME/KEY: misc_feature
```

Input Set : **A:\EP.txt**
Output Set: **N:\CRF3\04112002\J016516.raw**

```
   595 <222> LOCATION: (49)
   596 <223> OTHER INFORMATION: The 'Xaa' indicator at position 49 indicates the absence of
an amino
   597       acid residue.
   599 <220> FEATURE:
   600 <221> NAME/KEY: misc_feature
   601 <222> LOCATION: (54)..(55)
   602 <223> OTHER INFORMATION: The 'Xaa' indicators at positions 54-55 indicate the absence
of
   603       amino acid residues.
   605 <220> FEATURE:
   606 <221> NAME/KEY: misc_feature
   607 <222> LOCATION: (65)..(66)
   608 <223> OTHER INFORMATION: The 'Xaa' indicators at positions 65-66 indicate the absence
of
   609       amino acid residues.
   611 <220> FEATURE:
   612 <221> NAME/KEY: misc_feature
   613 <222> LOCATION: (101)
   614 <223> OTHER INFORMATION: The 'Xaa' indicator at position 101 indicates the absence of
an
   615       amino acid residue.
   617 <220> FEATURE:
   618 <221> NAME/KEY: misc_feature
   619 <222> LOCATION: (103)
   620 <223> OTHER INFORMATION: The 'Xaa' indicator at position 103 indicates the absence of
an
   621       amino acid residue.
   623 <220> FEATURE:
   624 <221> NAME/KEY: misc_feature
   625 <222> LOCATION: (121)..(127)
   626 <223> OTHER INFORMATION: The 'Xaa' indicators at positions 121-127 indicate the
absence of
   627       amino acid residues.
   629 <220> FEATURE:
   630 <221> NAME/KEY: misc_feature
   631 <222> LOCATION: (140)
   632 <223> OTHER INFORMATION: The 'Xaa' indicator at position 140 indicates the absence of
an
   633       amino acid residue.                    same
   635 <400> SEQUENCE: 10
W--> 636 Ala  Val  Lys  Leu  Val  Gln  Xaa  Ala  Gly  Xaa  Xaa  Gly  Xaa  Gly  Val  Val
E--> 637 Gln  Pro
E--> 638                                              1                        5
E--> 639 10                      15
W--> 641 Gly  Arg  Ser  Leu  Arg  Leu  Ser  Cys  Ile  Ala  Ser  Gly  Phe  Thr  Xaa  Xaa
E--> 642 Xaa  Xaa
E--> 643                                                                 20
E--> 644 25                 30            35
W--> 646 Xaa  Phe  Ser  Asn  Tyr  Gly  Met  His  Trp  Val  Arg  Gln  Xaa  Ala  Pro  Gly
E--> 647 Lys  Xaa
E--> 648                                                                 40
E--> 649 45                      50
```

```
W--> 651 Xaa  Gly  Leu  Glu  Trp  Val  Ala  Val  Ile  Trp  Xaa  Xaa  Tyr  Asn  Gly  Ser
E--> 652 Arg  Thr
E--> 653                                                    55                      60
```

Input Set : **A:\EP.txt**
Output Set: **N:\CRF3\04112002\J016516.raw**

```
E--> 654 65                         70
     656 Tyr Tyr Gly Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
E--> 657 Ser Lys
E--> 659 75                    80              85          90
W--> 661 Arg Thr Leu Tyr Met Gln Met Asn Ser Leu Xaa Arg Xaa Thr Glu Asp
E--> 662 Thr Alal
E--> 663                                                     95
E--> 664 100              105
W--> 666 Val Tyr Tyr Cys Ala Arg Asp Pro Asp Ile Leu Thr Xaa Xaa Xaa Xaa
E--> 667 Xaa Xaa
E--> 668                                                     110
E--> 669 115              120              125
W--> 671 Xaa Ala Phe Ser Phe Asp Tyr Trp Gly Gln Gly Val Leu Xaa Val Thr
E--> 672 Val Ser
E--> 673                                                     130
E--> 674 135              140
     676 <210> SEQ ID NO: 11
     677 <211> LENGTH: 144
     678 <212> TYPE: PRT
     679 <213> ORGANISM: 1VSC - Human Vcam-1
     681 <220> FEATURE:
     682 <221> NAME/KEY: misc_feature
     683 <222> LOCATION: (1)
     684 <223> OTHER INFORMATION: The 'Xaa' indicator at position 1 indicates the absence of
an amino
     685       acid residue.
     687 <220> FEATURE:
     688 <221> NAME/KEY: misc_feature
     689 <222> LOCATION: (7)
     690 <223> OTHER INFORMATION: The 'Xaa' indicator at position 7 indicates the absence of
an amino
     691       acid residue.
     693 <220> FEATURE:
     694 <221> NAME/KEY: misc_feature
     695 <222> LOCATION: (13)
     696 <223> OTHER INFORMATION: The 'Xaa' indicator at position 13 indicates the absence of
an amino
     697       acid residue.
     699 <220> FEATURE:
     700 <221> NAME/KEY: misc_feature
     701 <222> LOCATION: (33)..(39)
     702 <223> OTHER INFORMATION: The 'Xaa' indicators at positions 33-39 indicate the absence
of
     703       amino acid residues.
     706 <220> FEATURE:
     707 <221> NAME/KEY: misc_feature
     708 <222> LOCATION: (49)
     709 <223> OTHER INFORMATION: The 'Xaa' indicator at position 49 indicates the absence of
an amino
     710       acid residue.
     712 <220> FEATURE:
     713 <221> NAME/KEY: misc_feature
     714 <222> LOCATION: (52)..(77)
```

715 <223> OTHER INFORMATION: The 'Xaa' indicators at positions 52-77 indicate the absence
of

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716   amino acid residues.
718 <220> FEATURE:
719 <221> NAME/KEY: misc_feature
720 <222> LOCATION: (89)..(90)
721 <223> OTHER INFORMATION: The 'Xaa' indicators at positions 89-90 indicate the absence
of
722   amino acid residues.
724 <220> FEATURE:
725 <221> NAME/KEY: misc_feature
726 <222> LOCATION: (101)
727 <223> OTHER INFORMATION: The 'Xaa' indicator at position 101 indicates the absence of
an
728   amino acid residue.
730 <220> FEATURE:
731 <221> NAME/KEY: misc_feature
732 <222> LOCATION: (103)
733 <223> OTHER INFORMATION: The 'Xaa' indicator at position 103 indicates the absence of
an
734   amino acid residue.
736 <220> FEATURE:
737 <221> NAME/KEY: misc_feature
738 <222> LOCATION: (118)..(129)
739 <223> OTHER INFORMATION: The 'Xaa' indicators at positions 118-129 indicate the
absence of
740   amino acid residues.
742 <220> FEATURE:
743 <221> NAME/KEY: misc_feature
744 <222> LOCATION: (136)
745 <223> OTHER INFORMATION: The 'Xaa' indicator at position 136 indicates the absence of
an
746   amino acid residue.
748 <220> FEATURE:
749 <221> NAME/KEY: misc_feature
750 <222> LOCATION: (140)
751 <223> OTHER INFORMATION: The 'Xaa' indicator at position 140 indicates the absence of
an
752   amino acid residue.
754 <400> SEQUENCE: 11
W--> 755 Xaa Phe Lys Ile Glu Thr Xaa Thr Pro Glu Ser Arg Xaa Tyr Leu Ala
E--> 756 Gln Ile
E--> 757   1   5
E--> 758 10   15
W--> 760 Gly Asp Ser Val Ser Leu Thr Cys Ser Thr Thr Gly Cys Glu Xaa Xaa
E--> 761 Xaa Xaa
E--> 762   20
E--> 763 25   30   35
W--> 765 Xaa Xaa Xaa Ser Pro Phe Phe Ser Trp Arg Thr Gln Xaa Ile Asp Xaa
E--> 766 Xaa Xaa
E--> 767   40   45
E--> 768 50
W--> 770 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
E--> 771 Xaa Xaa
E--> 772   55   60

```
E--> 773 65                      70
W--> 775 Xaa  Xaa  Xaa  Xaa  Xaa  Ser  Pro  Leu  Asn  Gly  Lys  Val  Thr  Asn  Glu  Gly
```

Input Set : **A:\EP.txt**
Output Set: **N:\CRF3\04112002\J016516.raw**

```
E--> 776 Xaa  Xaa
E--> 777                                                                    75
E--> 778 80              85              90
W--> 780 Thr  Thr  Ser  Thr  Leu  Thr  Met  Asn  Pro  Val  Xaa  Ser  Xaa  Phe  Gly  Asn
E--> 781 Glu  His
E--> 782                                                              95
E--> 783 100             105
W--> 785 Ser  Tyr  Leu  Cys  Thr  Ala  Thr  Cys  Glu  Xaa  Xaa  Xaa  Xaa  Xaa  Xaa  Xaa
E--> 786 Xaa  Xaa
E--> 787                                                              110
E--> 788 115             120             125
W--> 790 Xaa  Xaa  Xaa  Ser  Arg  Lys  Leu  Glu  Lys  Xaa  Gly  Ile  Gln  Xaa  Val  Glu
E--> 791 Ile  Tyr
E--> 792                                                  130             135
E--> 793 140
```

same errors as Seq. 12

```
    900 <210> SEQ ID NO: 13
    901 <211> LENGTH: 144
    902 <212> TYPE: PRT
    903 <213> ORGANISM: 1F97 - Soluble Part of the Junction Adhesion Molecule from a Mouse
    905 <220> FEATURE:
    906 <221> NAME/KEY: misc_feature
    907 <222> LOCATION: (7)
    908 <223> OTHER INFORMATION: The 'Xaa' indicator at position 7 indicates the absence of
an amino
    909      acid residue.
    911 <220> FEATURE:
    912 <221> NAME/KEY: misc_feature
    913 <222> LOCATION: (11)
    914 <223> OTHER INFORMATION: The 'Xaa' indicator at position 11 indicates the absence of
an amino
    915      acid residue.
    917 <220> FEATURE:
    918 <221> NAME/KEY: misc_feature
    919 <222> LOCATION: (13)
    920 <223> OTHER INFORMATION: The 'Xaa' indicator at position 13 indicates the absence of
an amino
    921      acid residue.
    923 <220> FEATURE:
    924 <221> NAME/KEY: misc_feature
    925 <222> LOCATION: (33)..(39)
    926 <223> OTHER INFORMATION: The 'Xaa' indicators at positions 33-39 indicate the absence
of
    927      amino acid residues.
    929 <220> FEATURE:
    930 <221> NAME/KEY: misc_feature
    931 <222> LOCATION: (49)
    932 <223> OTHER INFORMATION: The 'Xaa' indicator at position 49 indicates the absence of
an amino
    933      acid residue
    935 <220> FEATURE:
    936 <221> NAME/KEY: misc_feature
    937 <222> LOCATION: (51)
    938 <223> OTHER INFORMATION: The 'Xaa' indicator at position 51 indicates the absence of
```

an amino
939   acid residue.

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        Input Set : A:\EP.txt
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    941 <220> FEATURE:
    942 <221> NAME/KEY: misc_feature
    943 <222> LOCATION: (54)..(55)
    944 <223> OTHER INFORMATION: The 'Xaa' indicators at positions 54-55 indicate the absence
of
    945   amino acid residues
    947 <220> FEATURE:
    948 <221> NAME/KEY: misc_feature
    949 <222> LOCATION: (65)..(72)
    950 <223> OTHER INFORMATION: The 'Xaa' indicators at positions 65-72 indicate the absence
of
    951   amino acid residues.
    953 <220> FEATURE:
    954 <221> NAME/KEY: misc_feature
    955 <222> LOCATION: (87)..(92)
    956 <223> OTHER INFORMATION: The 'Xaa' indicators at positions 87-92 indicate the absence
of
    957   amino acid residues.
    959 <220> FEATURE:
    960 <221> NAME/KEY: misc_feature
    961 <222> LOCATION: (101)
    962 <223> OTHER INFORMATION: The 'Xaa' indicator at position 101 indicates the absence of
an
    963   amino acid residue
    965 <220> FEATURE:
    966 <221> NAME/KEY: misc_feature   use apostrophe marks
    967 <222> LOCATION: (103)
    968 <223> OTHER INFORMATION: The (Xaa) indicator at position 103 indicates the absence of
an
    969   amino acid residue.
    971 <220> FEATURE:
    972 <221> NAME/KEY: misc_feature
    973 <222> LOCATION: (121)..(131)
    974 <223> OTHER INFORMATION: The 'Xaa' indicators at positions 121-131 indicate the
absence of
    975   amino acid residues.
    977 <220> FEATURE:
    978 <221> NAME/KEY: misc_feature
    979 <222> LOCATION: (140)
    980 <223> OTHER INFORMATION: The 'Xaa' indicator at position 140 indicates the absence of
an
    981   amino acid residue.
    983 <400> SEQUENCE: 13   same error
W--> 984 Lys Gly Ser Val Tyr Thr Xaa Ala Gln Ser Xaa Asp Xaa Val Gln Val
E--> 985 Pro Glu
E--> 986   1   5
E--> 987 10   15
W--> 989 Asn Glu Ser Ile Lys Leu Thr Cys Thr Tyr Ser Gly Phe Ser Xaa Xaa
E--> 990 Xaa Xaa
E--> 991   20
E--> 992 25   30   35
W--> 993 Xaa Xaa Xaa Ser Pro Arg Val Glu Trp Lys Phe Val Xaa Gln Xaa Gly
E--> 994 Ser Xaa

```
E--> 995                                                   40                    45
E--> 996 50
W--> 998 Xaa  Thr  Thr  Ala  Leu  Val  Cys  Tyr  Asn  Ser  Xaa  Xaa  Xaa  Xaa  Xaa  Xaa
```

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Input Set : **A:\EP.txt**
Output Set: **N:\CRF3\04112002\J016516.raw**

```
E--> 999 Xaa   Xaa
E--> 1000                                                           55
E--> 1001 60                    65             70
W--> 1003 Gln   Ile   Thr   Ala   Pro   Tyr   Ala   Asp   Arg   Val   Thr   Phe   Ser   Ser   Xaa   Xaa
E--> 1004 Xaa   Xaa
E--> 1005                                                           75
E--> 1006 80                    85             90
W--> 1008 Xaa   Xaa   Ser   Gly   Ile   Thr   Phe   Ser   Ser   Val   Xaa   Thr   Xaa   Arg   Lys   Asp
E--> 1009 Asn   Gly
E--> 1010                                                           95
E--> 1011 100                   105
W--> 1013 Glu   Tyr   Thr   Cys   Met   Val   Ser   Asx   Glu   Gly   Gly   Gln   Xaa   Xaa   Xaa   Xaa
E--> 1014 Xaa   Xaa
E--> 1015                                                           110
E--> 1016 115                   120                  125
W--> 1018 Xaa   Xaa   Xaa   Xaa   Xaa   Asn   Tyr   Gly   Glu   Val   Ser   Ile   His   Xaa   Leu   Thr
E--> 1019 Val   Leu
E--> 1020                                              130            135
E--> 1021 140
     1230 <210> SEQ ID NO: 16
     1231 <211> LENGTH: 144
     1232 <212> TYPE: PRT
     1233 <213> ORGANISM: 1IAR - Human Interleukin-4 Receptor Alpha Chain Complex
     1235 <220> FEATURE:
     1236 <221> NAME/KEY: misc_feature
     1237 <222> LOCATION: (7)
     1238 <223> OTHER INFORMATION: The 'Xaa' indicator at position 7 indicates the absence of
an amino
     1239       acid residue.
     1241 <220> FEATURE:
     1242 <221> NAME/KEY: misc_feature
     1243 <222> LOCATION: (12)..(16)
     1244 <223> OTHER INFORMATION: The 'Xaa' indicators at positions 12-16 indicate the
absence of
     1245       amino acid residues.
     1247 <220> FEATURE:
     1248 <221> NAME/KEY: misc_feature
     1249 <222> LOCATION: (49)
     1250 <223> OTHER INFORMATION: The 'Xaa' indicator at position 49 indicates the absence of
an amino
     1251       acid residue.
     1253 <220> FEATURE:
     1254 <221> NAME/KEY: misc_feature
     1255 <222> LOCATION: (54)..(55)
     1256 <223> OTHER INFORMATION: The 'Xaa' indicators at positions 54-55 indicate the
absence of
     1257       amino acid residues.
     1259 <220> FEATURE:
     1260 <221> NAME/KEY: misc_feature
     1261 <222> LOCATION: (65)..(90)
     1262 <223> OTHER INFORMATION: The 'Xaa' indicators at positions 65-90 indicate the
absence of
     1263       amino acid residues.
```

same error in seqs. 14-15

1265 <220> FEATURE:

```
     1266 <221> NAME/KEY: misc_feature
     1267 <222> LOCATION: (101)
     1268 <223> OTHER INFORMATION: The 'Xaa' indicator at position 101 indicates the absence
of an
     1269       amino acid residue.
     1271 <220> FEATURE:
     1272 <221> NAME/KEY: misc_feature
     1273 <222> LOCATION: (122)..(128)
     1274 <223> OTHER INFORMATION: The 'Xaa' indicators at positions 122-128 indicate the
absence of
     1275       amino acid residues.
     1277 <220> FEATURE:
     1278 <221> NAME/KEY: misc_feature
     1279 <222> LOCATION: (141)
     1280 <223> OTHER INFORMATION: The 'Xaa' indicator at position 141 indicates the absence
of an
     1281       amino acid residue.
     1285 <400> SEQUENCE: 16
W--> 1286 Arg  Ala  Pro  Gly  Asn  Leu  Xaa  Thr  Val  Asn  Thr  Xaa  Xaa  Xaa  Xaa  Xaa
E--> 1287 Asn  Val
E--> 1288                                                    1                  5
E--> 1289 10                  15
     1291 Ser  Asp  Thr  Leu  Leu  Leu  Thr  Trp  Ser  Asn  Pro  Tyr  Pro  Pro  Asp  Asn
E--> 1292 Tyr  Leu
E--> 1293                                                                       20
E--> 1294 25                  30                  35
W--> 1296 Tyr  Asn  His  Leu  Thr  Tyr  Ala  Val  Asn  Ile  Ser  Glu  Xaa  Asn  Asp  Pro
E--> 1297 Ala  Xaa
E--> 1298                                                                       40
E--> 1299 45                       50
W--> 1301 Xaa  Asp  Glu  Arg  Ile  Tyr  Asn  Val  Thr  Tyr  Xaa  Xaa  Xaa  Xaa  Xaa  Xaa
E--> 1302 Xaa  Xaa
E--> 1303                                                    55                 60
E--> 1304 65                       70
W--> 1306 Xaa  Xaa  Xaa  Xaa  Xaa  Xaa  Xaa  Xaa  Xaa  Xaa  Xaa  Xaa  Xaa  Xaa  Xaa  Xaa
E--> 1307 Xaa  Xaa
E--> 1308                                                                       75
E--> 1309 80                       85                  90
W--> 1311 Leu  Glu  Pro  Ser  Leu  Arg  Ile  Ala  Ala  Ser  Xaa  Thr  Leu  Lys  Ser  Gly
E--> 1312 Ile  Ser
E--> 1313                                                                       95
E--> 1314 100                 105
W--> 1316 Tyr  Arg  Ala  Arg  Val  Arg  Ala  Trp  Ala  Gln  Ala  Tyr  Asn  Xaa  Xaa  Xaa
E--> 1317 Xaa  Xaa
E--> 1318                                                                       110
E--> 1319 115                 120                 125
W--> 1321 Xaa  Xaa  Thr  Thr  Trp  Ser  Glu  Trp  Ser  Pro  Ser  Thr  Lys  Trp  Xaa  His
E--> 1322 Asn  Ser
E--> 1323                                                                       130
E--> 1324 135                 140
     1444 <210> SEQ ID NO: 18
     1445 <211> LENGTH: 363
```

same error (handwritten annotation near line 1285)

same error in seg. 17 (handwritten annotation near line 1324)

last sequence in file (handwritten annotation near bottom)

```
      1446 <212> TYPE: DNA
C--> 1447 <213> ORGANISM: Artificial
      1449 <220> FEATURE:
      1450 <221> NAME/KEY: misc_feature
      1451 <223> OTHER INFORMATION: Artificial Sequence: Exemplary primary scaffold used to
obtain
      1452         optimal secondary
      1453         scaffolds.
      1455 <220> FEATURE:
      1456 <221> NAME/KEY: misc_feature
      1457 <222> LOCATION: (73)..(99)
      1458 <223> OTHER INFORMATION: The nucleotide at positions 73-99 may be any nucleotide.
      1460 <220> FEATURE:
      1461 <221> NAME/KEY: misc_feature
      1462 <222> LOCATION: (157)..(177)
      1463 <223> OTHER INFORMATION: The nucleotide at positions 157-177 may be any nucleotide.
      1465 <220> FEATURE:
      1466 <221> NAME/KEY: misc_feature
      1467 <222> LOCATION: (292)..(333)
      1468 <223> OTHER INFORMATION: The nucleotide at positions 292-333 may be any nucleotide
      1470 <400> SEQUENCE: 18
E--> 1472 aat   gtg   aaa   ctg   gtt   gaa   aaa   ggt   ggc   aat   ttc   gtc   gaa
      1473 aac   gat   gac   gat   ctt         54
      1475 Asn   Val   Lys   Leu   Val   Glu   Lys   Gly   Gly   Asn   Phe   Val   Glu   Asn   Asp   Asp
W--> 1476 Asp   Leu
W--> 1477                                           1                 5
E--> 1478 10                  15
E--> 1480 aag   ctc   acg   tgc   cgt   gct   nnn   nnn   nnn   nnn   nnn   nnn   nnn   nnn
W--> 1481 nnn   atg   ggt   tgg 108
W--> 1483 Lys   Leu   Thr   Cys   Arg   Ala   Xaa   Xaa   Xaa   Xaa   Xaa   Xaa   Xaa   Xaa   Xaa   Met
W--> 1484 Gly   Trp
W--> 1485                                                             20
E--> 1486 25                  30                  35
E--> 1488 ttc   cgt   cag   gcg   ccg   aac   gac   gac   agt   act   aac   gtg   gcc
W--> 1489 acc   atc   gac   nnn   nnn   162
      1491 Phe   Arg   Gln   Ala   Pro   Asn   Asp   Asp   Ser   Thr   Asn   Val   Ala   Thr   Ile   Asp
W--> 1492 Xaa   Xaa
W--> 1493                                           40                45
E--> 1494 50
E--> 1496 nnn   nnn   nnn   nnn   nnn   tac   ggt   gac   tcc   gtc   aaa   gag   cgc
      1497 ttc   gat   atc   cgt   cgc   216
W--> 1499 Xaa   Xaa   Xaa   Xaa   Xaa   Tyr   Gly   Asp   Ser   Val   Lys   Glu   Arg   Phe   Asp   Ile
W--> 1500 Arg   Arg
W--> 1501                                           55
E--> 1502 60                  65                  70
E--> 1504 gac   aaa   ggc   tcc   aac   acc   gtt   acc   tta   tcg   atg   gac   gat
      1505 ctg   caa   ccg   gaa   gac   270
      1507 Asp   Lys   Gly   Ser   Asn   Thr   Val   Thr   Leu   Ser   Met   Asp   Asp   Leu   Gln   Pro
W--> 1508 Glu   Asp
W--> 1509                                                             75
```

RAW SEQUENCE LISTING   DATE: 04/11/2002
PATENT APPLICATION: US/10/016,516   TIME: 13:20:26

Input Set : A:\EP.txt
Output Set: N:\CRF3\04112002\J016516.raw

```
E--> 1510 80                    85                   90
E--> 1512 tct   gca   gaa   tac   aat   tgt   gca   nnn   nnn   nnn   nnn   nnn   nnn
W--> 1513 nnn   nnn   nnn   nnn   nnn   324
W--> 1515 Ser   Ala   Glu   Tyr   Asn   Cys   Ala   Xaa   Xaa   Xaa   Xaa   Xaa   Xaa   Xaa   Xaa   Xaa
W--> 1516 Xaa   Xaa
W--> 1517                                                                        95
E--> 1518 100                   105
E--> 1521 nnn   nnn   nnn   ggt   cag   ggt   acc   gac   gtt   acc   gtc   tcg   tcg
     1522 363
W--> 1524 Xaa   Xaa   Xaa   Gly   Gln   Gly   Thr   Asp   Val   Thr   Val   Ser   Ser
W--> 1525                                                       110               115
E--> 1526 120
```

same

FYI Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence using n or Xaa.

VERIFICATION SUMMARY
PATENT APPLICATION: **US/10/016,516**

DATE: 04/11/2002
TIME: 13:20:27

Input Set : **A:\EP.txt**
Output Set: **N:\CRF3\04112002\J016516.raw**

```
L:43  M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:39 SEQ:1
L:48  M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:49  M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
M:254 Repeated in SeqNo=1
L:52  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:55  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:56  M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:57  M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:61  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:64  M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:64  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:65  M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:69  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:72  M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:72  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:73  M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:76  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:79  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:80  M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:81  M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:89  M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:102 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:39 SEQ:2
L:106 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:120 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:39 SEQ:3
L:124 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:125 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
M:254 Repeated in SeqNo=3
L:132 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:133 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:140 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:141 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:148 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:149 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:156 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:157 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:164 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:165 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:172 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:173 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:181 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:193 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:39 SEQ:4
L:197 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
L:198 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
M:254 Repeated in SeqNo=4
L:205 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
L:206 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
L:213 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
L:214 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
```

VERIFICATION SUMMARY
PATENT APPLICATION: **US/10/016,516**

DATE: 04/11/2002
TIME: 13:20:27

Input Set : **A:\EP.txt**
Output Set: **N:\CRF3\04112002\J016516.raw**

```
L:221 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
L:222 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
L:229 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
L:230 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
L:237 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
L:238 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
L:245 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
L:246 M:252 E: No. of Seq. differs, <211>LENGTH:Input:422 Found:363 SEQ:4
L:258 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:39 SEQ:5
L:262 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:263 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
M:254 Repeated in SeqNo=5
L:270 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:271 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:278 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:279 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:286 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:287 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:294 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:295 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:412 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:413 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:8
M:332 Repeated in SeqNo=8
L:417 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:418 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:422 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:423 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:427 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:437 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:447 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:524 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:525 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:9
M:332 Repeated in SeqNo=9
L:529 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:534 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:535 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:539 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:549 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:554 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:555 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:559 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:636 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:637 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:10
M:332 Repeated in SeqNo=10
L:641 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:642 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:646 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:647 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:651 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
```